SEQUENCE LISTING

<110> Darrow, Andrew
Qi, Jenson
Andrade-Gordon, Patricia

<120> DNA ENCODING THE HUMAN SERINE PROTEASE T

<130> ORT-1560

<140> 10/041,054
<141> 2002-01-07

<150> 09/386,653
<151> 1999-08-31

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<170> PatentIn version 3.3

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<212> DNA
<213> Homo sapiens

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ccaggatgct gaaccgaatg gtgggcgggc aggacacgca ggagggcgag tggccctggc 180

aagtcagcat ccagcgcaac ggaagccact tctgcggggg cagcctcatc gcggagcagt 240

gggtcctgac ggctgcgcac tgcttccgca acacctctga gacgtccctg taccaggtcc 300

tgctgggggc aaggcagcta gtgcagccgg gaccacacgc tatgtatgcc cgggtgaggc 360

aggtggagag caacccccctg taccagggca cggcctccag cgctgacgtg gccctggtgg 420

agctggaggc accagtgccc ttcaccaatt acatcctccc cgtgtgcctg cctgacccct 480

cggtgatctt tgagacgggc atgaactgct gggtcactgg ctggggcagc cccagtgagg 540

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ccaagtgcaa cctgctctac agcaaagaca ccgagtttgg ctaccaaccc aaaaccatca 660

agaatgacat gctgtgcgcc ggcttcgagg agggcaagaa ggatgcctgc aagggcgact 720

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ggggtgaggg ctgtgcccgc cagaaccgcc caggtgtcta catccgtgtc accgcccacc 840

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agaagtgaga ccccggggc caggagcccc ttgagcagag ctctgcaccc agcctgcccg 960

cccacaccat cctgctggtc ctcccagcgc tgctgttgca cctgtgagcc ccaccagact 1020

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35 40 45

Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu
50 55 60

Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr
65 70 75 80

Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val
85 90 95

Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser
100 105 110

Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val
115 120 125

Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys
130 135 140

Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val
145 150 155 160

Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg
165 170 175

Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn
180 185 190

Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile
195 200 205

Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala
210 215 220

Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser
225 230 235 240

Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln
245 250 255

Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile
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Gln Lys
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gtggacgcgg ccgctcttgc tgccccctttt gatgatgatg acaagatcgt tgggggctat 180

gctctagagg agggcgagtg gccctggcaa gtcagcatcc agcgcaacgg aagccacttc 240

tgcgggggca gcctcatcgc ggagcagtgg gtcctgacgg ctgcgcactg cttccgcaac 300

acctctgaga cgtccctgta ccaggtcctg ctgggggcaa ggcagctagt gcagccggga 360

ccacacgcta tgtatgcccg ggtgaggcag gtggagagca acccccctgta ccagggcacg 420

gcctccagcg ctgacgtggc cctggtggag ctggaggcac cagtgccctt caccaattac 480

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gtcactggct ggggcagccc cagtgaggaa gacctcctgc ccgaaccgcg gatcctgcag 600

aaactcgctg tgcccatcat cgacacaccc aagtgcaacc tgctctacag caaagacacc 660

gagtttggct accaacccaa aaccatcaag aatgacatgc tgtgcgccgg cttcgaggag 720

ggcaagaagg atgcctgcaa gggcgactcg ggcggccccc tggtgtgcct cgtgggtcag 780

tcgtggctgc aggcgggggt gatcagctgg ggtgagggct gtgcccgcca gaaccgccca 840

ggtgtctaca tccgtgtcac cgcccaccac aactggatcc atcggatcat ccccaaactg 900

cagttccagc cagcgaggtt gggcggccag aagtctagac atcaccatca ccatcactag 960

cggccgcttc cctttagtga gggttaatgc ttcgagcaga catgataaga tacattgatg 1020

agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt gaaatttgtg 1080

atgctattgc tttatttgta accattataa gctgcaataa acaagttgac 1130

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Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Gly Glu Trp Pro
50 55 60

Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser
65 70 75 80

Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn
85 90 95

Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu
100 105 110

Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu
115 120 125

Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu
130 135 140

Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val
145 150 155 160

Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp
165 170 175

Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro
180 185 190

Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys
195 200 205

Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr
210 215 220

Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp
225 230 235 240

Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln
245 250 255

Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg
260 265 270

Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp
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Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly
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Gly Gln Lys Ser Arg His His His His His His
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Xaa Ala Pro Xaa

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